RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/680,963A
Source: IFW0
Date Processed by STIC: 5-26-05

ENTERED

IFWO

RAW SEQUENCE LISTING DATE: 05/26/2005
PATENT APPLICATION: **US/10/680,963A** TIME: 10:30:14

Input Set : **A:\GFI-108 Sequence listing.ST25**
Output Set: **N:\CRF4\05262005\J680963A.raw**

```
  3 <110> APPLICANT: GlycoFi, Inc.
  4       Bobrowicz, Piotr
  5       Hamilton, Stephen R.
  6       Gerngross, Tilman U.
  7       Wildt, Stefan
  8       Choi, Byung-Kwon
  9       Nett, Juergen H.
 10       Davidson, Robert C.
 12 <120> TITLE OF INVENTION: N-Acetylglucosaminyltransferase III expression in lower
 13       eukaryotes
 15 <130> FILE REFERENCE: GFI-108 CIP
 17 <140> CURRENT APPLICATION NUMBER: US 10/680,963A
 18 <141> CURRENT FILING DATE: 2003-10-07
 20 <150> PRIOR APPLICATION NUMBER: US 10/371,877
 21 <151> PRIOR FILING DATE: 2003-02-20
 23 <150> PRIOR APPLICATION NUMBER: US 09/892,591
 24 <151> PRIOR FILING DATE: 2001-06-27
 26 <150> PRIOR APPLICATION NUMBER: US 60/214,358
 27 <151> PRIOR FILING DATE: 2000-06-28
 29 <150> PRIOR APPLICATION NUMBER: US 60/215,638
 30 <151> PRIOR FILING DATE: 2000-06-30
 32 <150> PRIOR APPLICATION NUMBER: US 60/279,997
 33 <151> PRIOR FILING DATE: 2001-03-30
 35 <150> PRIOR APPLICATION NUMBER: PCT/US02/41510
 36 <151> PRIOR FILING DATE: 2002-12-24
 38 <150> PRIOR APPLICATION NUMBER: US 60/344,169
 39 <151> PRIOR FILING DATE: 2001-12-27
 41 <160> NUMBER OF SEQ ID NOS: 101
 43 <170> SOFTWARE: PatentIn version 3.2
 45 <210> SEQ ID NO: 1
W--> 46 <400> SEQUENCE: 1
W--> 47 000
 50 <210> SEQ ID NO: 2
W--> 51 <400> SEQUENCE: 2
W--> 52 000
 55 <210> SEQ ID NO: 3
 56 <211> LENGTH: 21
 57 <212> TYPE: DNA
 58 <213> ORGANISM: artificial
 60 <220> FEATURE:
 61 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,6-
mannosyltransferase)
 63 <400> SEQUENCE: 3
 64 atggcgaagg cagatggcag t                                          21
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(pg. 6)

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     68 <211> LENGTH: 21
     69 <212> TYPE: DNA
     70 <213> ORGANISM: artificial
     72 <220> FEATURE:
     73 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,6-
mannosyltransferase)
     75 <400> SEQUENCE: 4
     76 ttagtccttc caacttcctt c                                            21
     79 <210> SEQ ID NO: 5
     80 <211> LENGTH: 26
     81 <212> TYPE: DNA
     82 <213> ORGANISM: artificial
     84 <220> FEATURE:
     85 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,2
     86       mannosyltransferases)
     89 <220> FEATURE:
     90 <221> NAME/KEY: misc_feature
     91 <222> LOCATION: (9)..(9)
     92 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
     94 <220> FEATURE:
     95 <221> NAME/KEY: misc_feature
     96 <222> LOCATION: (12)..(12)
     97 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
     99 <220> FEATURE:
    100 <221> NAME/KEY: misc_feature
    101 <222> LOCATION: (18)..(18)
    102 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
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W--> 105 taytggmgng tngarcynga yathaa                                      26
    108 <210> SEQ ID NO: 6
    109 <211> LENGTH: 20
    110 <212> TYPE: DNA
    111 <213> ORGANISM: artificial
    113 <220> FEATURE:
    114 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,2
    115       mannosyltransferases)
    118 <220> FEATURE:
    119 <221> NAME/KEY: misc_feature
    120 <222> LOCATION: (6)..(6)
    121 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
    123 <220> FEATURE:
    124 <221> NAME/KEY: misc_feature
    125 <222> LOCATION: (12)..(12)
    126 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
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W--> 129 gcrtcncccc anckytcrta                                             20
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W--> 133 <400> SEQUENCE: 7
W--> 134 000
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Input Set : **A:\GFI-108 Sequence listing.ST25**
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W--> 138 <400> SEQUENCE: 8
W--> 139 000
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    143 <211> LENGTH: 458
    144 <212> TYPE: PRT
    145 <213> ORGANISM: Saccharomyces cerevisiae
    147 <400> SEQUENCE: 9
    149 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
    150 1               5                  10                  15
    153 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
    154             20                  25                  30
    157 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
    158         35                  40                  45
    161 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
    162     50                  55                  60
    165 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
    166 65                  70                  75                  80
    169 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
    170                 85                  90                  95
    173 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
    174             100                 105                 110
    177 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
    178         115                 120                 125
    181 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
    182     130                 135                 140
    185 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
    186 145                 150                 155                 160
    189 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
    190                 165                 170                 175
    193 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
    194             180                 185                 190
    197 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
    198         195                 200                 205
    201 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
    202     210                 215                 220
    205 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
    206 225                 230                 235                 240
    209 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
    210                 245                 250                 255
    213 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
    214             260                 265                 270
    217 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
    218         275                 280                 285
    221 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
    222     290                 295                 300
    225 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
    226 305                 310                 315                 320
    229 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
```

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```
230                 325                 330                 335
233 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
234             340                 345                 350
237 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
238         355                 360                 365
241 Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
242     370                 375                 380
245 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
246 385                 390                 395                 400
249 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
250                 405                 410                 415
253 Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala
254             420                 425                 430
257 Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
258         435                 440                 445
261 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
262     450                 455
265 <210> SEQ ID NO: 10
266 <211> LENGTH: 458
267 <212> TYPE: PRT
268 <213> ORGANISM: Saccharomyces cerevisiae
270 <400> SEQUENCE: 10
272 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
273 1               5                   10                  15
276 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
277             20                  25                  30
280 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
281         35                  40                  45
284 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
285     50                  55                  60
288 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
289 65                  70                  75                  80
292 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
293                 85                  90                  95
296 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
297             100                 105                 110
300 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
301         115                 120                 125
304 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
305     130                 135                 140
308 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
309 145                 150                 155                 160
312 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
313                 165                 170                 175
316 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
317             180                 185                 190
320 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
321         195                 200                 205
324 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
```

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PATENT APPLICATION: US/10/680,963A TIME: 10:30:14

Input Set : A:\GFI-108 Sequence listing.ST25
Output Set: N:\CRF4\05262005\J680963A.raw

```
325     210                 215                 220
328 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
329 225                 230                 235                 240
332 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
333                 245                 250                 255
336 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
337             260                 265                 270
340 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
341         275                 280                 285
344 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
345     290                 295                 300
348 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
349 305                 310                 315                 320
352 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
353                 325                 330                 335
356 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
357             340                 345                 350
360 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
361         355                 360                 365
364 Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
365     370                 375                 380
368 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
369 385                 390                 395                 400
372 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
373                 405                 410                 415
376 Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala
377             420                 425                 430
380 Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
381         435                 440                 445
384 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
385     450                 455
388 <210> SEQ ID NO: 11
389 <211> LENGTH: 389
390 <212> TYPE: PRT
391 <213> ORGANISM: Saccharomyces cerevisiae
393 <400> SEQUENCE: 11
395 Trp Gln Asp Leu Lys Asp Gly Val Arg Tyr Val Ile Phe Asp Cys Arg
396 1               5                   10                  15
399 Ala Asn Leu Ile Val Met Pro Leu Leu Ile Leu Phe Glu Ser Met Leu
400             20                  25                  30
403 Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys
404         35                  40                  45
407 Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp
408     50                  55                  60
411 Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly
412 65                  70                  75                  80
415 His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp
416                 85                  90                  95
419 His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr
```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/26/2005
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Input Set : A:\GFI-108 Sequence listing.ST25
Output Set: N:\CRF4\05262005\J680963A.raw

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 9,12,18
Seq#:6; N Pos. 6,12
Seq#:75; N Pos. 17,20

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,41,42,47,48,49,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68
Seq#:69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,94,95,96
Seq#:97,98,99,100,101

VERIFICATION SUMMARY DATE: 05/26/2005
PATENT APPLICATION: **US/10/680,963A** TIME: 10:30:15

Input Set : **A:\GFI-108 Sequence listing.ST25**
Output Set: **N:\CRF4\05262005\J680963A.raw**

L:46 M:283 W: Missing Blank Line separator, <400> field identifier
L:47 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (1) SEQUENCE:
L:51 M:283 W: Missing Blank Line separator, <400> field identifier
L:52 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (2) SEQUENCE:
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:133 M:283 W: Missing Blank Line separator, <400> field identifier
L:134 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:138 M:283 W: Missing Blank Line separator, <400> field identifier
L:139 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:2445 M:283 W: Missing Blank Line separator, <400> field identifier
L:2446 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (43) SEQUENCE:
L:2450 M:283 W: Missing Blank Line separator, <400> field identifier
L:2451 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
L:3240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0